

SEQUENCE LISTING

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Aguiar, Ricardo
Yakushijin, Yoshi

<120> LYMPHOMA ASSOCIATED MOLECULES AND USES THEREFOR

<130> DFN-031US

<140> US 09/830,762

<141> 2001-04-27

<150> PCT/US99/25439

<151> 1999-10-29

<150> US 60/106,383

<151> 1998-10-29

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<170> PatentIn Ver. 2.0

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Glu Thr Gly Ala Leu Gly Glu Asn Tyr Ser Trp Gln Ile Pro Ile Asn	
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His Asn Asp Phe Lys Ile Leu Lys Asn Asn Glu Arg Gln Leu Cys Glu	
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Ile Ala Val Thr Gly Ala Gly Arg Leu Pro Cys Lys Gln Ile Ile His	
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Ala Gly Glu Ile Ala Val Thr Gly Ala Gly Arg Leu Pro Cys Lys Gln	
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cct	aaa	cct	cag	ata	tta	aaa	cat	gca	atg	aag	gag	tgt	ttg	gaa	aaa	1248	
Pro	Lys	Pro	Gln	Ile	Leu	Lys	His	Ala	Met	Lys	Glu	Cys	Leu	Glu	Lys		
				405					410					415			
tgc	att	gag	caa	aat	ata	act	tcc	att	tcc	ttt	cct	gcc	ctt	ggg	act	1296	
Cys	Ile	Glu	Gln	Asn	Ile	Thr	Ser	Ile	Ser	Phe	Pro	Ala	Leu	Gly	Thr		

420	425	430	
gga aac atg gaa ata aag aag gaa aca gca gca gag att ttg ttt gat Gly Asn Met Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp 435 440 445			1344
gaa gtt tta aca ttt gcc aaa gac cat gta aaa cac cag tta act gta Glu Val Leu Thr Phe Ala Lys Asp His Val Lys His Gln Leu Thr Val 450 455 460			1392
aaa ttt gtg atc ttt cca aca gat ttg gag ata tat aag gct ttc agt Lys Phe Val Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser 465 470 475 480			1440
tct gaa atg gca aag agg tcc aag atg ctg agt ttg aac aat tac agt Ser Glu Met Ala Lys Arg Ser Lys Met Leu Ser Leu Asn Asn Tyr Ser 485 490 495			1488
gtc ccc cag tca acc aga gag gag aaa aga gaa aat ggg ctt gaa gct Val Pro Gln Ser Thr Arg Glu Glu Lys Arg Glu Asn Gly Leu Glu Ala 500 505 510			1536
aga tct cct gcc atc aat ctg atg gga ttc aac gtg gaa gag atg tat Arg Ser Pro Ala Ile Asn Leu Met Gly Phe Asn Val Glu Glu Met Tyr 515 520 525			1584
gag gcc cac gca tgg atc caa aga atc ctg agt ctc cag aac cac cac Glu Ala His Ala Trp Ile Gln Arg Ile Leu Ser Leu Gln Asn His His 530 535 540			1632
atc att gag aat aat cat att ctg tac ctt ggg aga aag gaa cat gac Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Arg Lys Glu His Asp 545 550 555 560			1680
att ttg tct cag ctt cag aaa act tca agt gtc tcc atc aca gaa att Ile Leu Ser Gln Leu Gln Lys Thr Ser Ser Val Ser Ile Thr Glu Ile 565 570 575			1728
atc agc cca gga agg aca gag tta gag att gaa gga gcc cgg gct gac Ile Ser Pro Gly Arg Thr Glu Leu Glu Ile Glu Gly Ala Arg Ala Asp 580 585 590			1776
ctc att gag gtg gtt atg aac att gaa gat atg ctt tgt aaa gta cag Leu Ile Glu Val Val Met Asn Ile Glu Asp Met Leu Cys Lys Val Gln 595 600 605			1824
gag gaa atg gca agg aaa aag gag cga ggc ctt tgg cgc tcg tta gga Glu Glu Met Ala Arg Lys Lys Glu Arg Gly Leu Trp Arg Ser Leu Gly 610 615 620			1872
cag tgg act att cag caa caa aaa acc caa gac gaa atg aaa gaa aat Gln Trp Thr Ile Gln Gln Gln Lys Thr Gln Asp Glu Met Lys Glu Asn 625 630 635 640			1920

atc ata ttt ctg aaa tgt cct gtg cct cca act caa gag ctt cta gat	1968
Ile Ile Phe Leu Lys Cys Pro Val Pro Pro Thr Gln Glu Leu Leu Asp	
645 650 655	
caa aag aaa cag ttt gaa aaa tgt ggt ttg cag gtt cta aag gtg gag	2016
Gln Lys Lys Gln Phe Glu Lys Cys Gly Leu Gln Val Leu Lys Val Glu	
660 665 670	
aag ata gac aat gag gtc ctt atg gct gcc ttt caa aga aag aag aaa	2064
Lys Ile Asp Asn Glu Val Leu Met Ala Ala Phe Gln Arg Lys Lys Lys	
675 680 685	
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Met Met Glu Glu Lys Leu His Arg Gln Pro Val Ser His Arg Leu Phe	
690 695 700	
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Gln Gln Val Pro Tyr Gln Phe Cys Asn Val Val Cys Arg Val Gly Phe	
705 710 715 720	
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Gln Arg Met Tyr Ser Thr Pro Cys Asp Pro Lys Tyr Gly Ala Gly Ile	
725 730 735	
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Tyr Phe Thr Lys Asn Leu Lys Asn Leu Ala Glu Lys Ala Lys Lys Ile	
740 745 750	
tct gct gca gat aag ctg atc tat gtg ttt gag gct gaa gta ctc aca	2304
Ser Ala Ala Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr	
755 760 765	
ggc ttc ttc tgc cag gga cat ccg tta aat att gtt ccc cca cca ctg	2352
Gly Phe Phe Cys Gln Gly His Pro Leu Asn Ile Val Pro Pro Pro Leu	
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Ser Pro Gly Ala Ile Asp Gly His Asp Ser Val Val Asp Asn Val Ser	
785 790 795 800	
agc cct gaa acc ttt gtt att ttt agt ggc atg cag gct ata cct cag	2448
Ser Pro Glu Thr Phe Val Ile Phe Ser Gly Met Gln Ala Ile Pro Gln	
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Tyr Leu Trp Thr Cys Thr Gln Glu Tyr Val Gln Ser Gln Asp Tyr Ser	
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Ser Gly Pro Met Arg Pro Phe Ala Gln His Pro Trp Arg Gly Phe Ala	
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Ser Gly Ser Pro Val Asp	
850	

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Ala Gly Arg Leu Pro Cys His Leu Ile Ile His Ala Val Gly Pro Arg
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Trp Thr Val Thr Asn Ser Gln Thr Ala Ile Glu Leu Leu Lys Phe Ala	
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Ile Arg Asn Ile Leu Asp Tyr Val Thr Lys Tyr Asp Leu Arg Ile Lys	
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aca gta gca att cca gcc ctg agc tct gga att ttc cag ttc cct ctg	800
Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile Phe Gln Phe Pro Leu	
195 200 205 210	
gat ttg tgt aca agc ata att tta gaa act atc cgg ctt tat ttc caa	848
Asp Leu Cys Thr Ser Ile Ile Leu Glu Thr Ile Arg Leu Tyr Phe Gln	
215 220 225	
gac aag caa atg ttc ggt aat ttg aga gag att cat ctg gtg agc aat	896
Asp Lys Gln Met Phe Gly Asn Leu Arg Glu Ile His Leu Val Ser Asn	
230 235 240	
gag gac ccc act gtt gcg tcc ttt aaa tcc gcc tca gaa agc atc cta	944
Glu Asp Pro Thr Val Ala Ser Phe Lys Ser Ala Ser Glu Ser Ile Leu	
245 250 255	
ggg agg gac ctg agc tct tgg ggg ggt cca gaa act gac cct gct tcc	992
Gly Arg Asp Leu Ser Ser Trp Gly Gly Pro Glu Thr Asp Pro Ala Ser	
260 265 270	
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Thr Met Thr Leu Arg Ile Gly Arg Gly Leu Thr Leu Gln Ile Val Gln	
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Gly Cys Ile Glu Met Gln Thr Thr Asp Val Ile Gly Asn Ser Gly Tyr	
295 300 305	
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Ala Gly Val Glu Met Glu Lys Glu Leu Asp Lys Val Asn Leu Ser Thr	
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Asp Tyr Gln Glu Val Trp Val Thr Lys Gly Phe Lys Leu Ser Cys Gln	
340 345 350	
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Tyr Val Phe His Val Ala Trp His Ser Gln Ile Asn Lys Tyr Gln Ile	
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Leu Lys Asp Ala Met Lys Ser Cys Leu Glu Lys Cys Leu Lys Pro Asp	
375 380 385	

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Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met Asp Leu	
390 395 400	
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Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe Ala Phe	
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gct aaa gag cac aag gaa aaa acg cta act gta aag att gtg atc ttt	1472
Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val Ile Phe	
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cca gta gat gtg gag acg tac aag att ttt tat gct gaa atg aca aaa	1520
Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met Thr Lys	
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Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu Ala Leu	
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Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala Gly Ser	
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Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys Glu Ala	
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Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His Ile Ile	
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Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp Val Leu	
515 520 525 530	
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Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr Val Ser	
535 540 545	
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Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp Leu Ile	
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gac gca gtt atg agg att gaa tgt atg ctg tgt gac gtt cag gaa gaa	1904
Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln Glu Glu	
565 570 575	
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Val Ala Gly Lys Arg Glu Lys Asn Leu Trp Ser Leu Ser Gly Gln Gly	
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acc aac cag caa gaa aaa ctg gat aaa atg gaa gaa tcg tac aca ttt	2000
Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr Thr Phe	
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<211> 826

<212> PRT

<213> Murinae gen. sp.

<400> 5

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Glu	Ile	Leu	Lys	Ser	Asn	Glu	Ser	Gln	Leu	Cys	Glu	Val	Leu	Gln	Asn	35	40	45	
Lys	Phe	Gly	Cys	Ile	Ser	Thr	Leu	Ser	Cys	Pro	Thr	Leu	Ala	Gly	Ser	50	55	60	
Ser	Ser	Pro	Ala	Gln	Arg	Val	Phe	Arg	Arg	Thr	Leu	Ile	Pro	Gly	Ile	65	70	75	80
Glu	Leu	Ser	Val	Trp	Lys	Asp	Asp	Leu	Thr	Arg	His	Val	Val	Asp	Ala	85	90	95	
Val	Val	Asn	Ala	Ala	Asn	Glu	Asn	Leu	Leu	His	Gly	Ser	Gly	Leu	Ala	100	105	110	
Gly	Ser	Leu	Val	Lys	Thr	Gly	Gly	Phe	Glu	Ile	Gln	Glu	Glu	Ser	Lys	115	120	125	
Arg	Ile	Ile	Ala	Asn	Val	Gly	Lys	Ile	Ser	Val	Gly	Gly	Ile	Ala	Ile	130	135	140	
Thr	Gly	Ala	Gly	Arg	Leu	Pro	Cys	His	Leu	Ile	Ile	His	Ala	Val	Gly	145	150	155	160
Pro	Arg	Trp	Thr	Val	Thr	Asn	Ser	Gln	Thr	Ala	Ile	Glu	Leu	Leu	Lys	165	170	175	
Phe	Ala	Ile	Arg	Asn	Ile	Leu	Asp	Tyr	Val	Thr	Lys	Tyr	Asp	Leu	Arg	180	185	190	
Ile	Lys	Thr	Val	Ala	Ile	Pro	Ala	Leu	Ser	Ser	Gly	Ile	Phe	Gln	Phe	195	200	205	

Pro 210	Leu	Asp	Leu	Cys	Thr	Ser 215	Ile	Ile	Leu	Glu	Thr 220	Ile	Arg	Leu	Tyr
Phe 225	Gln	Asp	Lys	Gln	Met 230	Phe	Gly	Asn	Leu	Arg 235	Glu	Ile	His	Leu	Val 240
Ser	Asn	Glu	Asp	Pro 245	Thr	Val	Ala	Ser	Phe 250	Lys	Ser	Ala	Ser	Glu 255	Ser
Ile	Leu	Gly	Arg 260	Asp	Leu	Ser	Ser	Trp 265	Gly	Gly	Pro	Glu	Thr 270	Asp	Pro
Ala	Ser	Thr 275	Met	Thr	Leu	Arg	Ile 280	Gly	Arg	Gly	Leu	Thr 285	Leu	Gln	Ile
Val	Gln 290	Gly	Cys	Ile	Glu	Met 295	Gln	Thr	Thr	Asp	Val 300	Ile	Gly	Asn	Ser
Gly 305	Tyr	Met	Gln	Asp	Phe 310	Lys	Ser	Gly	Arg	Val 315	Ala	Gln	Ser	Ile	Leu 320
Arg	Gln	Ala	Gly	Val 325	Glu	Met	Glu	Lys	Glu 330	Leu	Asp	Lys	Val	Asn 335	Leu
Ser	Thr	Asp	Tyr 340	Gln	Glu	Val	Trp	Val 345	Thr	Lys	Gly	Phe	Lys 350	Leu	Ser
Cys	Gln 355	Tyr	Val	Phe	His	Val	Ala 360	Trp	His	Ser	Gln	Ile 365	Asn	Lys	Tyr
Gln 370	Ile	Leu	Lys	Asp	Ala	Met 375	Lys	Ser	Cys	Leu	Glu 380	Lys	Cys	Leu	Lys
Pro 385	Asp	Ile	Asn	Ser	Ile 390	Ser	Phe	Pro	Ala	Leu 395	Gly	Thr	Gly	Leu	Met 400
Asp	Leu	Lys	Lys	Ser 405	Thr	Ala	Ala	Gln	Ile 410	Met	Phe	Glu	Glu	Val 415	Phe
Ala	Phe	Ala	Lys 420	Glu	His	Lys	Glu	Lys 425	Thr	Leu	Thr	Val	Lys 430	Ile	Val
Ile	Phe 435	Pro	Val	Asp	Val	Glu	Thr 440	Tyr	Lys	Ile	Phe	Tyr 445	Ala	Glu	Met
Thr 450	Lys	Arg	Ser	Asn	Glu	Leu 455	Asn	Leu	Ser	Gly	Asn 460	Ser	Gly	Ala	Leu
Ala 465	Leu	Gln	Trp	Ser	Ser 470	Gly	Glu	Gln	Arg	Arg 475	Gly	Gly	Leu	Glu	Ala 480
Gly	Ser	Pro	Ala	Ile 485	Asn	Leu	Met	Gly	Val 490	Lys	Val	Gly	Glu	Met 495	Cys
Glu	Ala	Gln	Glu 500	Trp	Ile	Glu	Arg	Leu 505	Leu	Val	Ser	Leu	Asp 510	His	His

Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp
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 530 535 540
 Val Ser Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp
 545 550 555 560
 Leu Ile Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln
 565 570 575
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 580 585 590
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 595 600 605
 Thr Phe Gln Arg Tyr Pro Ala Ser Leu Thr Gln Glu Leu Gln Asp Arg
 610 615 620
 Lys Lys Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln
 625 630 635 640
 Ile Asp Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met
 645 650 655
 Met Glu Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln
 660 665 670
 Gln Val Pro His Gln Phe Cys Asn Thr Val Cys Arg Val Gly Phe His
 675 680 685
 Arg Met Tyr Ser Thr Ser Tyr Asn Pro Val Tyr Gly Ala Gly Ile Tyr
 690 695 700
 Phe Thr Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser
 705 710 715 720
 Ser Thr Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly
 725 730 735
 Ser Phe Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser
 740 745 750
 Pro Gly Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser
 755 760 765
 Pro Glu Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr
 770 775 780
 Leu Trp Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp
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Trp Glu Trp Val Leu Asn Gly Ser Ser Val
820 825

<210> 6

<211> 2478

<212> DNA

<213> Murinae gen. sp.

<220>

<221> CDS

<222> (1)..(2478)

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ctt gaa gaa cat tat aga tgg caa att ccc att aaa cac aat gtc ttc	96
Leu Glu Glu His Tyr Arg Trp Gln Ile Pro Ile Lys His Asn Val Phe	
20 25 30	
gaa att tta aag agc aat gag agt cag cta tgt gaa gtc ctc caa aat	144
Glu Ile Leu Lys Ser Asn Glu Ser Gln Leu Cys Glu Val Leu Gln Asn	
35 40 45	
aag ttt gga tgc atc tct acc ctg agc tgt cca act cta gca ggg agc	192
Lys Phe Gly Cys Ile Ser Thr Leu Ser Cys Pro Thr Leu Ala Gly Ser	
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Ser Ser Pro Ala Gln Arg Val Phe Arg Arg Thr Leu Ile Pro Gly Ile	
65 70 75 80	
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Glu Leu Ser Val Trp Lys Asp Asp Leu Thr Arg His Val Val Asp Ala	
85 90 95	
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Val Val Asn Ala Ala Asn Glu Asn Leu Leu His Gly Ser Gly Leu Ala	
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Gly Ser Leu Val Lys Thr Gly Gly Phe Glu Ile Gln Glu Glu Ser Lys	
115 120 125	
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Arg Ile Ile Ala Asn Val Gly Lys Ile Ser Val Gly Gly Ile Ala Ile	
130 135 140	
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Thr Gly Ala Gly Arg Leu Pro Cys His Leu Ile Ile His Ala Val Gly	
145 150 155 160	
cct cgg tgg aca gtt acg aac agc cag aca gct atc gaa tta ctg aaa	528

Pro	Arg	Trp	Thr	Val	Thr	Asn	Ser	Gln	Thr	Ala	Ile	Glu	Leu	Leu	Lys		
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Phe	Ala	Ile	Arg	Asn	Ile	Leu	Asp	Tyr	Val	Thr	Lys	Tyr	Asp	Leu	Arg		
			180					185					190				
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Ile	Lys	Thr	Val	Ala	Ile	Pro	Ala	Leu	Ser	Ser	Gly	Ile	Phe	Gln	Phe		
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cct	ctg	gat	ttg	tgt	aca	agc	ata	att	tta	gaa	act	atc	cgg	ctt	tat	672	
Pro	Leu	Asp	Leu	Cys	Thr	Ser	Ile	Ile	Leu	Glu	Thr	Ile	Arg	Leu	Tyr		
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Phe	Gln	Asp	Lys	Gln	Met	Phe	Gly	Asn	Leu	Arg	Glu	Ile	His	Leu	Val		
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Ser	Asn	Glu	Asp	Pro	Thr	Val	Ala	Ser	Phe	Lys	Ser	Ala	Ser	Glu	Ser		
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atc	cta	ggg	agg	gac	ctg	agc	tct	tgg	ggg	ggt	cca	gaa	act	gac	cct	816	
Ile	Leu	Gly	Arg	Asp	Leu	Ser	Ser	Trp	Gly	Gly	Pro	Glu	Thr	Asp	Pro		
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gct	tcc	acc	atg	act	ctt	cgc	atc	ggc	cgg	ggc	ctg	act	ctc	cag	att	864	
Ala	Ser	Thr	Met	Thr	Leu	Arg	Ile	Gly	Arg	Gly	Leu	Thr	Leu	Gln	Ile		
		275					280					285					
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	290					295				300							
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Ser	Thr	Asp	Tyr	Gln	Glu	Val	Trp	Val	Thr	Lys	Gly	Phe	Lys	Leu	Ser		
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Cys	Gln	Tyr	Val	Phe	His	Val	Ala	Trp	His	Ser	Gln	Ile	Asn	Lys	Tyr		
		355					360					365					
cag	ata	ttg	aaa	gat	gca	atg	aag	tcc	tgt	cta	gaa	aaa	tgc	ctt	aaa	1152	
Gln	Ile	Leu	Lys	Asp	Ala	Met	Lys	Ser	Cys	Leu	Glu	Lys	Cys	Leu	Lys		
	370					375					380						
cca	gat	ata	aat	tcc	att	tcc	ttt	cct	gct	ctc	ggg	aca	gga	ttg	atg	1200	
Pro	Asp	Ile	Asn	Ser	Ile	Ser	Phe	Pro	Ala	Leu	Gly	Thr	Gly	Leu	Met		

385	390	395	400	
gat ttg aag aag agt	aca gca gct cag	ata atg ttt gag	gaa gtt ttt	1248
Asp Leu Lys Lys Ser	Thr Ala Ala Gln	Ile Met Phe Glu	Glu Val Phe	
	405	410	415	
gca ttt gct aaa gag	cac aag gaa aaa	acg cta act gta	aag att gtg	1296
Ala Phe Ala Lys Glu	His Lys Glu Lys	Thr Leu Thr Val	Lys Ile Val	
	420	425	430	
atc ttt cca gta gat	gtg gag acg tac	aag att ttt tat	gct gaa atg	1344
Ile Phe Pro Val Asp	Val Glu Thr Tyr	Lys Ile Phe Tyr	Ala Glu Met	
	435	440	445	
aca aaa agg tcc aac	gag ctg aat ctc	agc ggt aat agt	ggt gct tta	1392
Thr Lys Arg Ser Asn	Glu Leu Asn Leu	Ser Gly Asn Ser	Gly Ala Leu	
	450	455	460	
gcc ctg cag tgg tcc	agt ggg gag caa	aga aga ggc ggc	ctt gaa gct	1440
Ala Leu Gln Trp Ser	Ser Gly Glu Gln	Arg Arg Gly Gly	Leu Glu Ala	
	465	470	475	480
gga tct cct gcc atc	aat ctc atg ggt	gta aaa gtg gga	gag atg tgt	1488
Gly Ser Pro Ala Ile	Asn Leu Met Gly	Val Lys Val Gly	Glu Met Cys	
	485	490	495	
gag gcc cag gaa tgg	att gaa agg ttg	ctg gtc tcc ctg	gac cac cac	1536
Glu Ala Gln Glu Trp	Ile Glu Arg Leu	Leu Val Ser Leu	Asp His His	
	500	505	510	
atc att gag aat aat	cat att ctc tat	ctt ggg aaa aaa	gag cac gac	1584
Ile Ile Glu Asn Asn	His Ile Leu Tyr	Leu Gly Lys Lys	Glu His Asp	
	515	520	525	
gtg ctg tct gag ctc	cag acc agc aca	aga gtc tcc att	tca gag act	1632
Val Leu Ser Glu Leu	Gln Thr Ser Thr	Arg Val Ser Ile	Ser Glu Thr	
	530	535	540	
gtc agt cca aga acg	gcc act ttg gag	att aaa ggt ccc	cag gct gac	1680
Val Ser Pro Arg Thr	Ala Thr Leu Glu	Ile Lys Gly Pro	Gln Ala Asp	
	545	550	555	560
ctc att gac gca gtt	atg agg att gaa	tgt atg ctg tgt	gac gtt cag	1728
Leu Ile Asp Ala Val	Met Arg Ile Glu	Cys Met Leu Cys	Asp Val Gln	
	565	570	575	
gaa gaa gtg gca gga	aaa agg gag aaa	aat ctt tgg agc	ttg tca gga	1776
Glu Glu Val Ala Gly	Lys Arg Glu Lys	Asn Leu Trp Ser	Leu Ser Gly	
	580	585	590	
cag ggg acc aac cag	caa gaa aaa ctg	gat aaa atg gaa	gaa tca tac	1824
Gln Gly Thr Asn Gln	Gln Glu Lys Leu	Asp Lys Met Glu	Glu Ser Tyr	
	595	600	605	
aca ttt caa cga tac	cca gca tca ttaact	cag gaa ctt cag	gac cga	1872
Thr Phe Gln Arg Tyr	Pro Ala Ser Leu	Thr Gln Glu Leu	Gln Asp Arg	
	610	615	620	

aag Lys 625	aaa Lys	cag Gln	ttt Phe	gaa Glu	aag Lys 630	tgt Cys	ggc Gly	ttg Leu	tgg Trp	gtt Val 635	gtg Val	cag Gln	gtg Val	gag Glu	cag Gln 640	1920
ata Ile	gac Asp	aat Asn	aag Lys	gtg Val 645	ctg Leu	ctg Leu	gct Ala	gcc Ala	ttc Phe 650	caa Gln	gag Glu	aag Lys	aag Lys	aaa Lys 655	atg Met	1968
atg Met	gaa Glu	gag Glu	agg Arg 660	acg Thr	cca Pro	aag Lys	gga Gly	tct Ser 665	ggg Gly	agc Ser	caa Gln	agg Arg	ttg Leu 670	ttt Phe	cag Gln	2016
cag Gln	gtc Val	cca Pro 675	cat His	cag Gln	ttc Phe	tgc Cys	aat Asn 680	acg Thr	gtg Val	tgc Cys	aga Arg	gtc Val 685	ggc Gly	ttc Phe	cac His	2064
aga Arg 690	atg Met	tat Tyr	tcg Ser	aca Thr	tcc Ser	tat Tyr 695	aac Asn	cca Pro	gtt Val	tat Tyr 700	gga Gly	gcc Ala	ggc Gly	ata Ile	tat Tyr	2112
ttc Phe 705	acc Thr	aag Lys	agc Ser	ctc Leu 710	aaa Lys	aat Asn	cta Leu	gca Ala	gac Asp 715	aag Lys 715	gtc Val	aag Lys	aaa Lys	acc Thr	tca Ser 720	2160
agc Ser	aca Thr	gac Asp	aag Lys	cta Leu 725	atc Ile	tat Tyr	gtg Val	ttt Phe	gag Glu 730	gca Ala	gaa Glu	gta Val	ctc Leu	aca Thr 735	ggg Gly	2208
tcc Ser	ttc Phe	tgt Cys	cag Gln 740	ggc Gly	aat Asn	tcc Ser	tca Ser 745	aat Asn	atc Ile	atc Ile	cct Pro	cca Pro	cca Pro 750	ttg Leu	agt Ser	2256
cct Pro	ggg Gly 755	gcc Ala	tta Leu	gat Asp	gtc Val	aat Asn	gac Asp 760	agc Ser	gta Val	gtt Val	gac Asp 765	aat Asn	gtt Val	tcc Ser	agc Ser	2304
cct Pro 770	gaa Glu	acc Thr	att Ile	gtt Val	gtt Val 775	ttt Phe	aat Asn	ggc Gly	atg Met	cag Gln	gcc Ala 780	atg Met	ccc Pro	ctg Leu	tac Tyr	2352
ttg Leu 785	tgg Trp	act Thr	tgc Cys	aca Thr 790	cag Gln	gat Asp	agg Arg	aca Thr	ttc Phe 795	tca Ser 795	cag Gln	cat His	ccg Pro	atg Met	tgg Trp 800	2400
tca Ser	cag Gln	gac Asp	tac Tyr	tca Ser 805	tca Ser	gga Gly	cca Pro	gga Gly	atg Met 810	gtc Val	tct Ser	tcg Ser	ctg Leu	cag Gln 815	tcc Ser	2448
tgg Trp	gaa Glu	tgg Trp	gtc Val 820	tta Leu	aat Asn	ggc Gly	agc Ser	tct Ser 825	gtt Val							2478